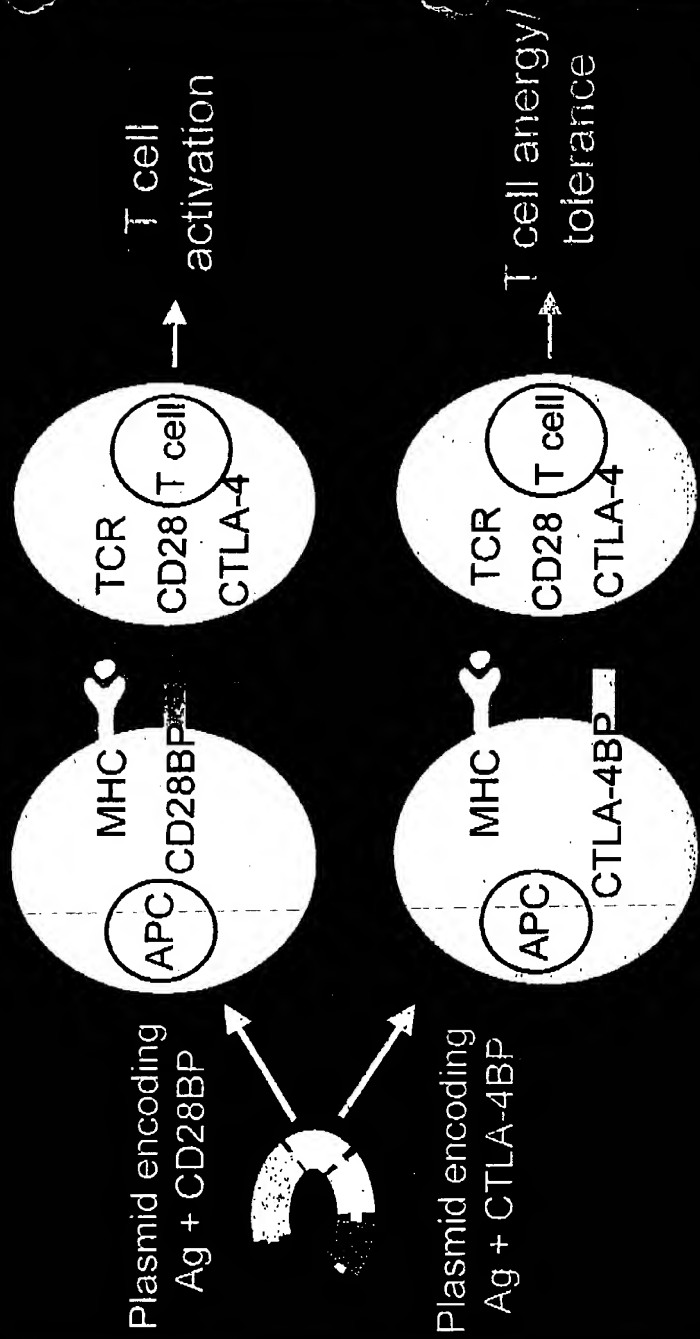


Altered T cell Function Evolved Ligand Binding



MA YGEN

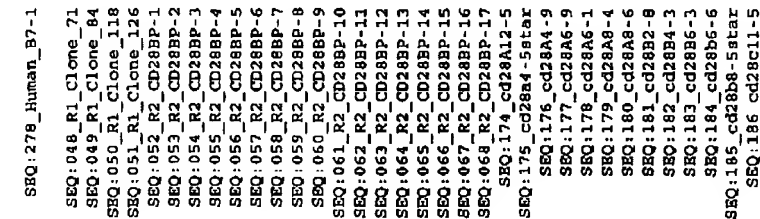
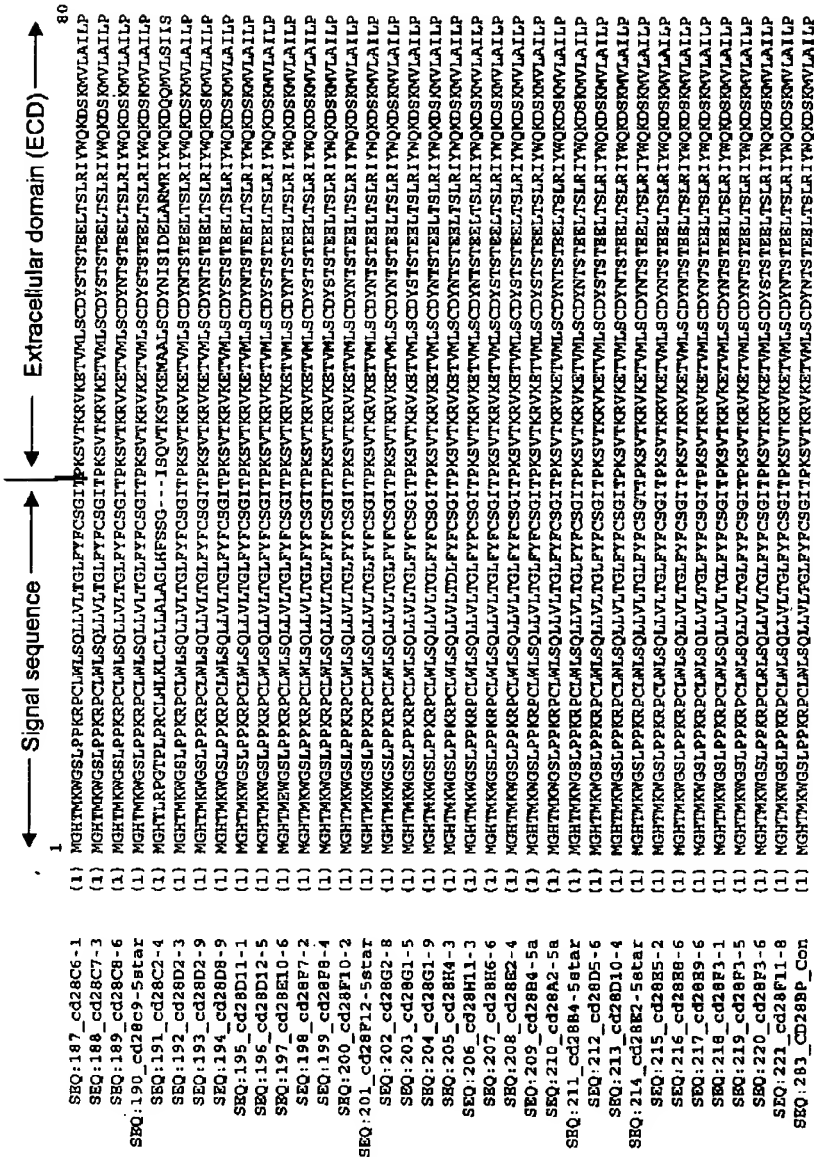


Fig. 2A



81	Extracellular domain (ECD)	160
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(79)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(80)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(81)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(82)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(83)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(84)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(85)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(86)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(87)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(88)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(89)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(90)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(91)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(92)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(93)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(94)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(95)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(96)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(97)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(98)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(99)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(100)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(101)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(102)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(103)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(104)
81	GDMNIPYKQRTITDNNLSIVIALRSDSGTTCVIOKPVLAGAYKLEHLASVRLMIRADFPVPTINDLGNPSNI	(105)

Fig. 2C

		←	Extracellular domain (ECD)	→	
SEQ:278_Human_B7-1	161	(158)	RRILCSTSGGPPRPHLYMLENGEELNANITTVSDPOTELYAVSSMLDPMNTNHSFACLIKYGHILAVNQTNNMTTKQB	240	
SEQ:048_R1_clone_71	(161)	RRILCSTSGGPPRPHLYMLENGEELNANITTVSDPOTELYAVSSMLDPMNTNHSFACLIKYGHILAVNQTNNMTTKQB			
SEQ:049_R1_clone_84	(157)	KRIICRSASGGPPRPLAMWEDGEEELNANITTVSDQDLOTELYSVSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:050_R1_clone_118	(157)	KRIICRSASGGPPRPLAMWEDGEEELNANITTVSDQDLOTELYSVSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:051_R1_clone_126	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:052_R2_CD28BP-1	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:053_R2_CD28BP-2	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:054_R2_CD28BP-3	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:055_R2_CD28BP-4	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:056_R2_CD28BP-5	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:057_R2_CD28BP-6	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:058_R2_CD28BP-7	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:059_R2_CD28BP-8	(161)	KRIICRSASGGPPRPLAMWEDGEEELNANITTVSDQDLOTELYSVSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:060_R2_CD28BP-9	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:061_R2_CD28BP-10	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:062_R2_CD28BP-11	(160)	KRIICRSASGGPPRPLAMWEDGEEELNANITTVSDQDLOTELYSVSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:063_R2_CD28BP-12	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDLOTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:064_R2_CD28BP-13	(161)	RRLICSTSGGPPRPLAMWEDGEEELNANITTVSDQDLOTELYSVSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:065_R2_CD28BP-14	(158)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:066_R2_CD28BP-15	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:067_R2_CD28BP-16	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:068_R2_CD28BP-17	(160)	KRIICRSASGGPPRPLAMWEDGEEELNANITTVSDQDLOTELYSVSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:174_cd28A12-5	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:175_cd28A4-5-6-7	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:176_cd28A4-9	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:177_cd28A6-9	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:178_cd28A6-1	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:179_cd28A8-4	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:180_cd28A8-6	(160)	KRIICRSASGGPPRPLAMWEDGEEELNANITTVSDQDLOTELYSVSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:181_cd28B2-8	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:182_cd28B4-3	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:183_cd28B6-3	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:184_cd28B6-6	(161)	KRIICRSASGGPPRPLAMWEDGEEELNANITTVSDQDLOTELYSVSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:185_cd28B8-5-6-7	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			
SEQ:186_cd38c11-5	(161)	RRLICSTSGGPPRPHLYMLENGEELNANITTVSDQDTELYMTSSLDPMNTNHSIVCLIKYGELSVSOIIPFMSKPKQB			

Fig. 2E

	←	Extracellular domain (ECD)	→	240
161				
SEQ: 187_cd28C6-1	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 188_cd28C7-3	(161)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 189_cd28C8-6	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 190_cd28C9-5star	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 191_cd28C2-4	(158)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 192_cd28D2-3	(159)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 193_cd28D2-9	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 194_cd28D8-9	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 195_cd28D11-1	(160)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 196_cd28D12-5	(161)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 197_cd28E10-6	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 198_cd28F7-2	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 199_cd28F8-4	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 200_cd28F10-2	(161)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 201_cd28F12-5star	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 202_cd28G2-8	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 203_cd28G1-5	(160)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 204_cd28G1-9	(161)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 205_cd28H4-3	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 206_cd28H11-3	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 207_cd28H6-6	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 208_cd28E2-4	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 209_cd28E4-5a	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 210_cd28A2-5a	(161)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 211_cd28B4-5star	(161)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 212_cd28D5-6	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 213_cd28D10-4	(160)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 214_cd28E2-5star	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 215_cd28E8-2	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 216_cd28E8-6	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 217_cd28E9-6	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 218_cd28F3-1	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 219_cd28F3-5	(160)	KRIRCSAGDPPRLAMWEDGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 220_cd28F3-6	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 221_cd28F11-8	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	
SEQ: 283_CD28BF_Con	(161)	RLICSTSGGPRPHLYWLENGELNATNTTTSQDPGTELYMISSSELDFTNNHSIVCLIKYGBLSVSOI	PPMSKPQOE	

Fig. 2F

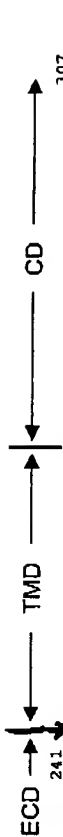
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Fig. 2G

"ECD → | ← TMD → | ← CD →" 307
 241
 SEQ:187_cd2806-1 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:188_cd2807-3 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:189_cd2808-6 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:190_cd2809-5star (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:191_cd2802-4 (238) P-SANOHLTWTIIIPVSAFGLSVIIIVLCLTCRCAAIRRRORRENEVMQSCQSP-----
 SEQ:192_cd2802-3 (239) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:193_cd2802-9 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:194_cd2808-9 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:195_cd2801-1 (240) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:196_cd2810-5 (238) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:197_cd2810-6 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:198_cd2807-2 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:199_cd2808-4 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:200_cd2802-2 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:201_cd2802-5star (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:202_cd2802-8 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:203_cd2801-5 (240) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:204_cd2801-9 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:205_cd2804-3 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:206_cd2801-1-3 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:207_cd2806-6 (238) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:208_cd2802-4 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:209_cd2804-3a (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:210_cd2802-5a (241) P-SANOHLTWTIIIPVSAFGLSVIIIVLCLTCRCAAIRRRORRENEVMQSCQSP-----
 SEQ:211_cd2804-5star (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:212_cd2805-6 (241) P-SANOHLTWTIIIPVSAFGLSVIIIVLCLTCRCAAIRRRORRENEVMQSCQSP-----
 SEQ:213_cd2801-4 (240) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:214_cd2802-5star (241) P-SANOHLTWTIIIPVSAFGLSVIIIVLCLTCRCAAIRRRORRENEVMQSCQSP-----
 SEQ:215_cd2805-2 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:216_cd2808-6 (241) P-SANOHLTWTIIIPVSAFGLSVIIIVLCLTCRCAAIRRRORRENEVMQSCQSP-----
 SEQ:217_cd2809-6 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:218_cd2803-1 (241) P-SANOHLTWTIIIPVSAFGLSVIIIVLCLTCRCAAIRRRORRENEVMQSCQSP-----
 SEQ:219_cd2803-5 (240) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:220_cd2803-6 (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG
 SEQ:221_cd2801-8 (238) P-SANOHLTWTIIIPVSAFGLSVIIIVLCLTCRCAAIRRRORRENEVMQSCQSP-----
 SEQ:283_CD280BP_Con (241) P-PIDQLPFVWIIIP---VSGALVLTAVVLYCLACRHHVAKKTRNEETVGTLSPIYLGSAQSSG

Fig. 2H

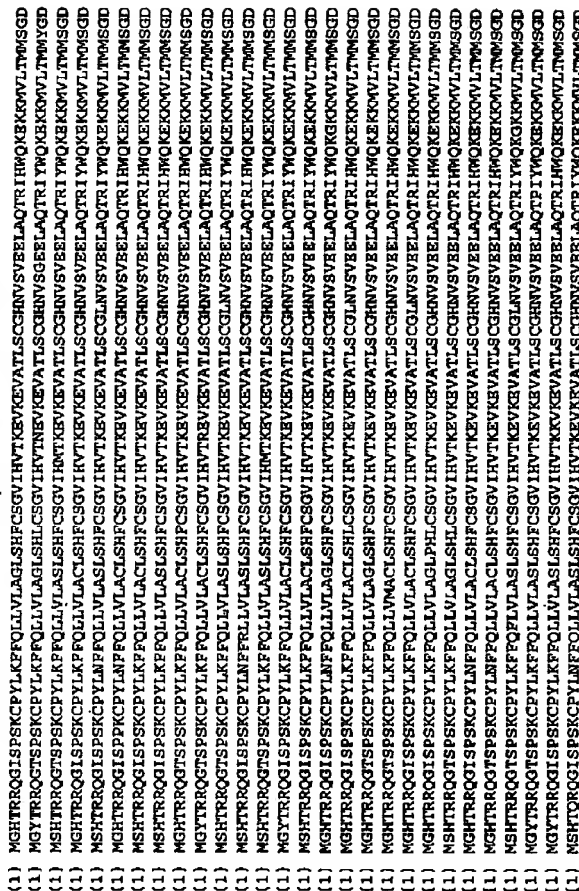


Fig. 3A

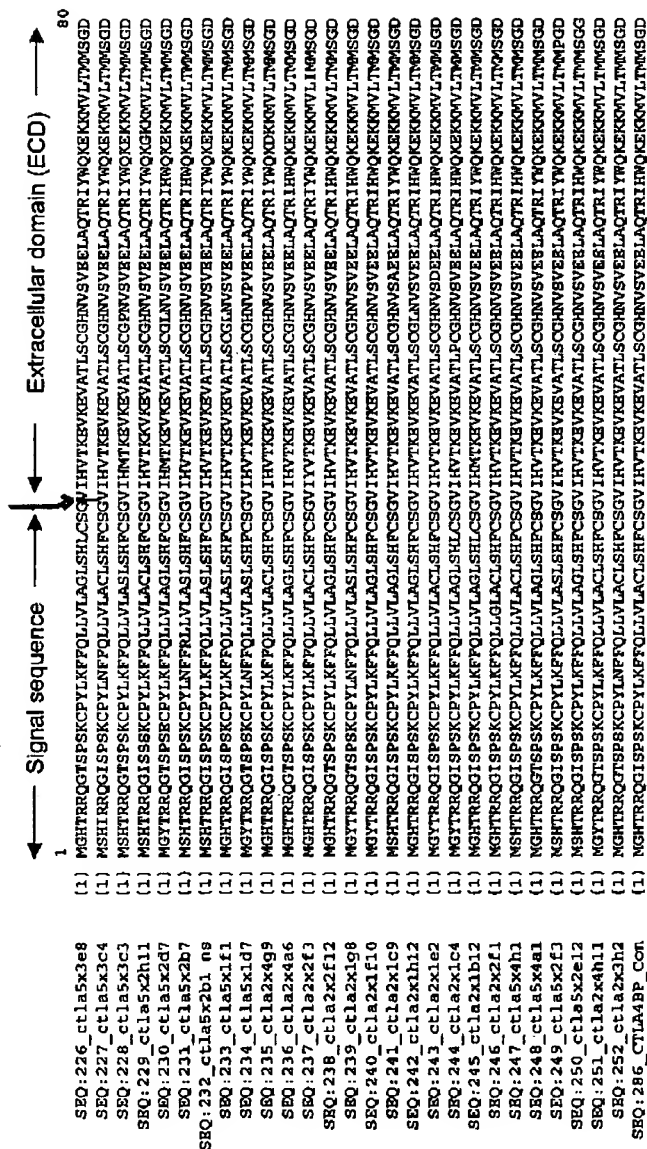


Fig. 3B

SEQ: 276 Human_B7-1

SEQ: 069_R1 CTLA4BP-5
SEQ: 070_R1 CTLA4BP-7
SEQ: 071_R1 CTLA4BP-11
SEQ: 072_R1 CTLA4BP-13
SEQ: 073_R1 CTLA4BP-27
SEQ: 074_R2 CTLA4BP-5x2-10C
SEQ: 075_R2 CTLA4BP-5x2-11D
SEQ: 076_R2 CTLA4BP-5x2-12F
SEQ: 077_R2 CTLA4BP-5x2-29G
SEQ: 078_R2 CTLA4BP-5x2-3C
SEQ: 079_R2 CTLA4BP-5x2-4C
SEQ: 080_R2 CTLA4BP-5x2-7b
SEQ: 081_R2 CTLA4BP-5x2-8C
SEQ: 082_R2 CTLA4BP-5x3-10e
SEQ: 083_R2 CTLA4BP-5x3-11b
SEQ: 084_R2 CTLA4BP-5x3-6f
SEQ: 085_R2 CTLA4BP-5x4-11D
SEQ: 086_R2 CTLA4BP-5x4-12C
SEQ: 087_R2 CTLA4BP-5x4-1f
SEQ: 088_R2 CTLA4BP-5x5-2e
SEQ: 089_R2 CTLA4BP-5x5-6e
SEQ: 090_R2 CTLA4BP-5x6-9d
SEQ: 091_R2 CTLA4BP-5x8-1f
SEQ: 092_R2 CTLA4BP-5x9-12C
SEQ: 222_ctla5x9d10
SEQ: 223_ctla5x6f6
SEQ: 224_ctla5x5h12
SEQ: 225_ctla5x5c10
SEQ: 226_ctla5x5c10

Extracellular domain (ECD)

[illegible]

Fig. 3C

160

[illegible]

Extracellular domain (ECD) \longleftrightarrow

240

Fig. 3F

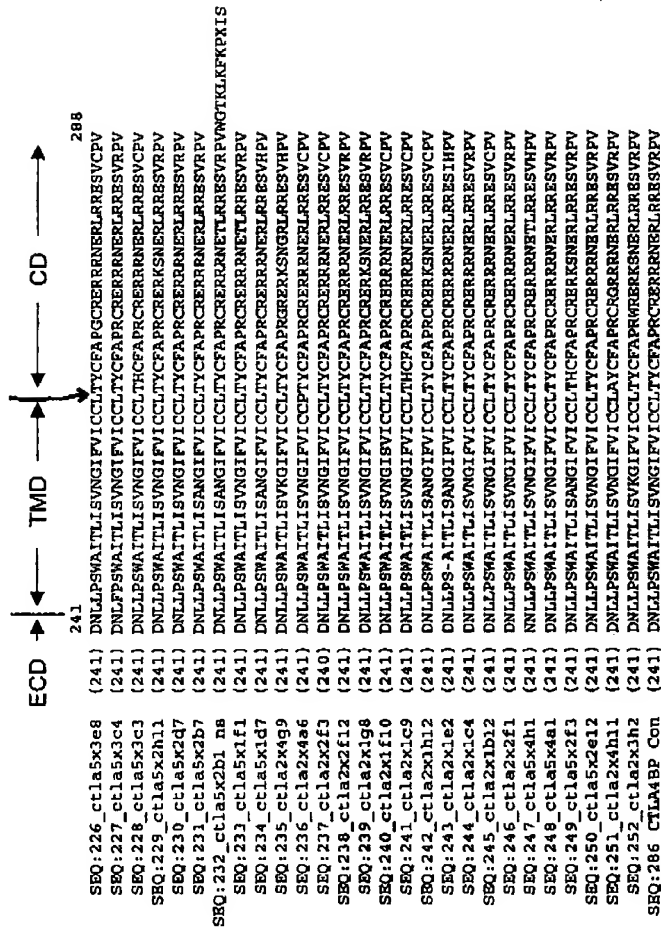


Fig. 3H

Figures 4A-4D

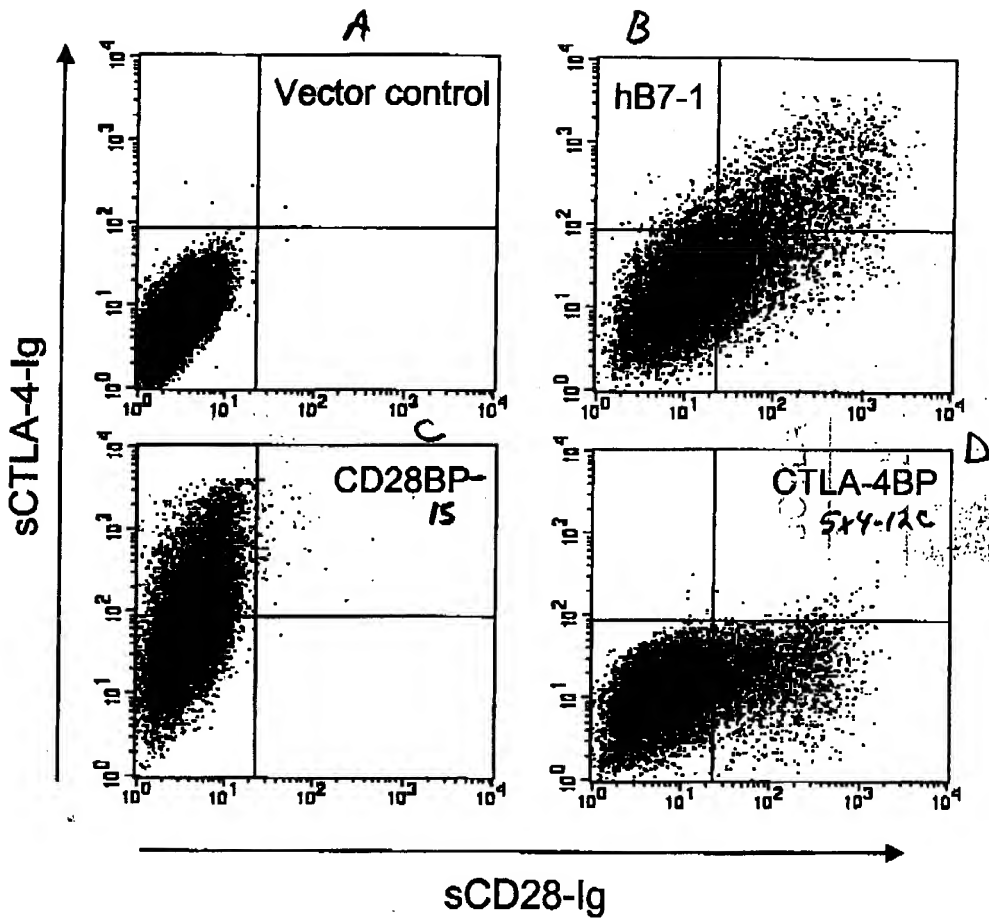
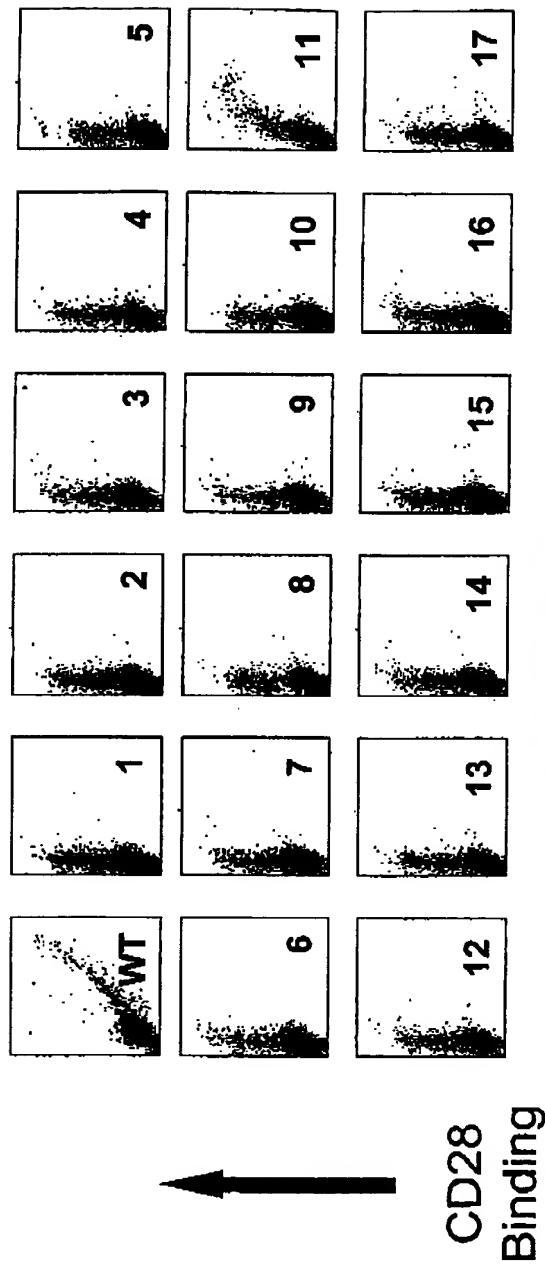


Figure 5

CD28BP after 2nd Round of Shuffling

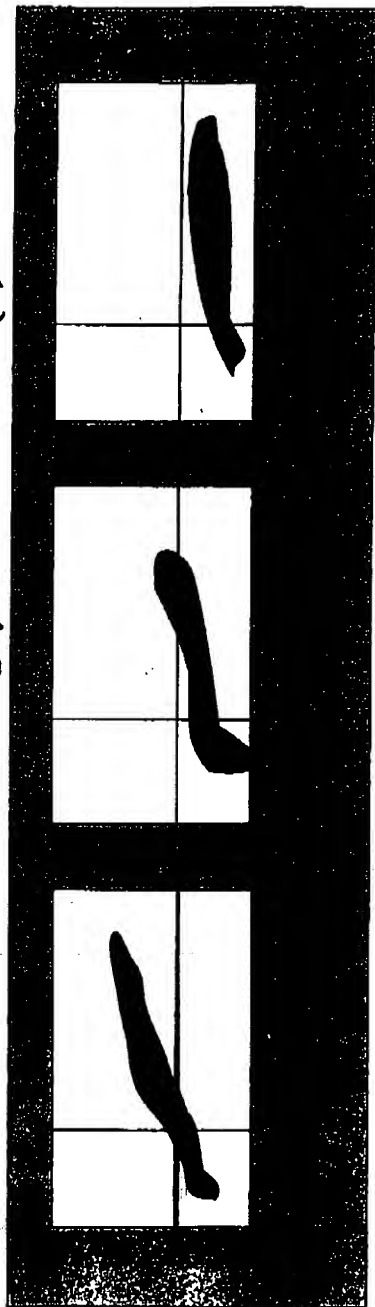


Figures A-LB.

A(1)

A(2)

A(3)



B(1) CTLA-4-Ig Binding

B(3)

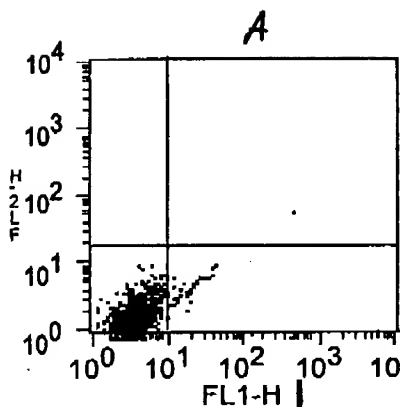
B(2)



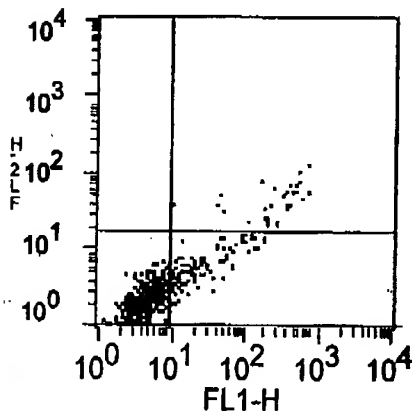
CTLA-4-Ig Binding →

Figures 1A-7D

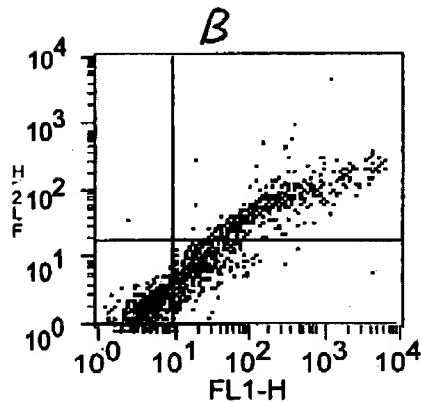
CD28 Binding (PE)



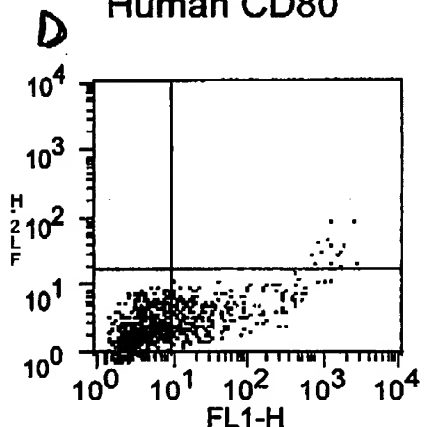
HEK 293



CTLA4BP R25X5-2E



Human CD80

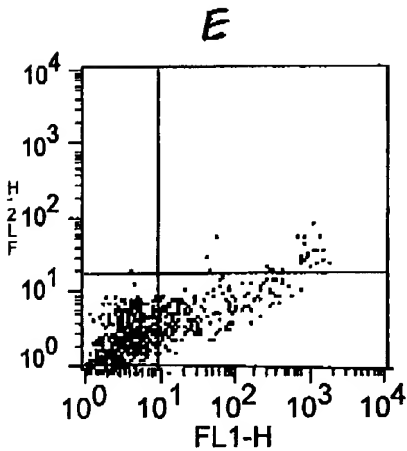


CTLA4BP R25X4-12C

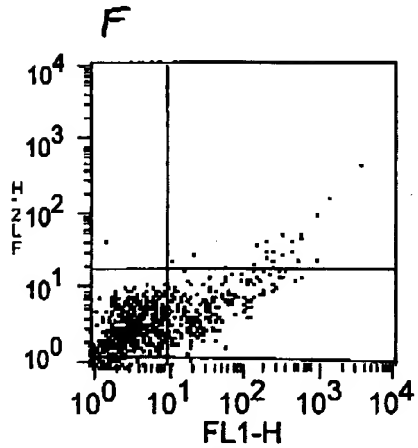
CTLA4 Binding (FITC)

Figures E-7H

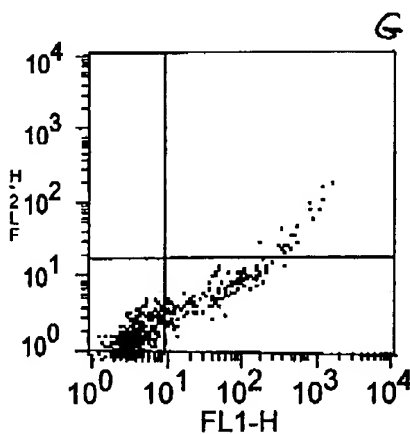
CD28 Binding (PE)



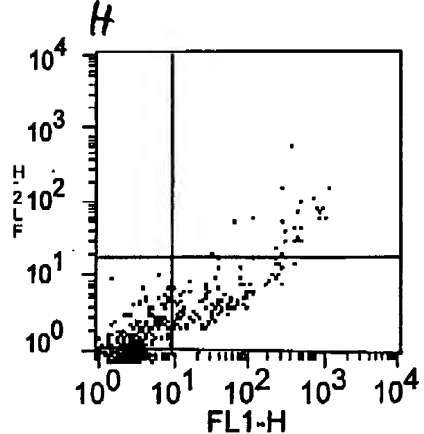
CTLA4BP R25X4-11D



CTLA4BP R25X2-8C



CTLA4BP R25X6-9D



CTLA4BP R25X8-1F

CTLA4 Binding (FITC)

a CTLA4BP-5x4-12c

MGHTRRQGTSPSKCPYLKFFQLLVLAGLSHFCSGVHVTKEVKEVATLSCGHNVSVVEELAQT
 K human → baboon ← human →
 RIHWQKEKQKMLVTMMSGDMNIWPEYKNRTIFDITNLSIVILALRPSDEGTCECWLKYEKDAF
 human → rhesus/baboon →
 KREHLAEVMSVKADFTPTSIDFEIPPSNIRRIICSTSGGFPEPHLFWLENGEELNAINTTVSQ
 rhesus/baboon → human → baboon →
 DPETELYTVSSKLDENMTTNHSMCLIKYGHILRVNQTFNWNTPKQEHFPDNLPSWAITLISA
 → rhesus
 NGIFVICCLTYRFAPRCRERKSNETLRRESVRPV
 human → orangutan → rhesus → baboon

b CD28BP-15

MGHTMKWGSLPPKRPCLWLSQLLVLTGLFYFCSGITPKSVTKRVKEIVMLSCDYNTSTEELT
 ← cow
 SLRIYWQKDSKMVLAILPGKVQVWPEYKNRTITDMNDNPRIVILALRPSDSGTYTCVIQKPVLK
 → cow
 GAYKLEHLASVRLMIRADFPVPTINDLGNPSPNIRRLICSTSGGFPRPHLYWLENGEELNATNT
 cow → human → cow
 TVSQDRTGTELYMISSLDENVTNHNSIVCLIKYGELSVSQIFPWSKPKQEPIDQLPEWVIVPS
 baboon → rabbit
 GALVLTAVLYCLACRHVARWKRTRNEETVGTERTSPIYLGSAQSSG

 human rhesus/baboon rabbit
 orangutan cow
 rhesus
 baboon cow

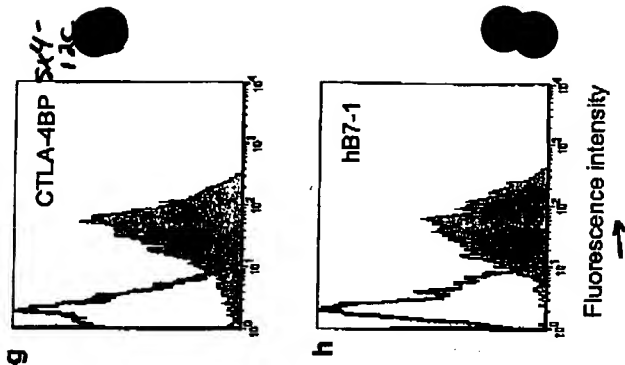
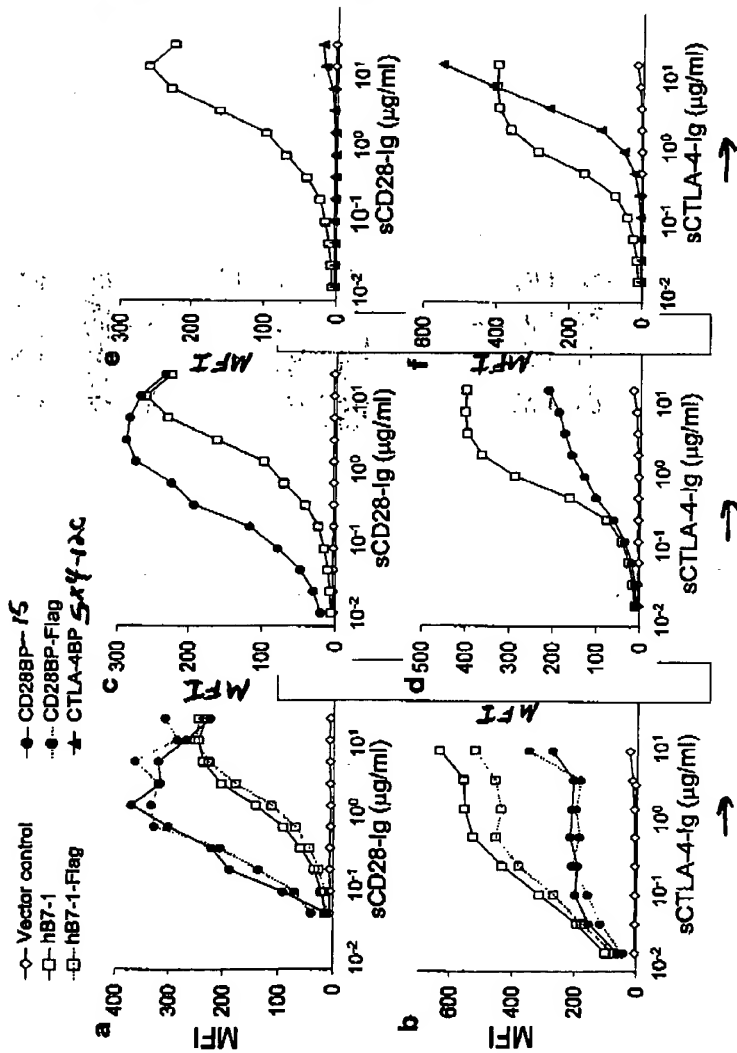


Figure 9A-9H

102250"4288860

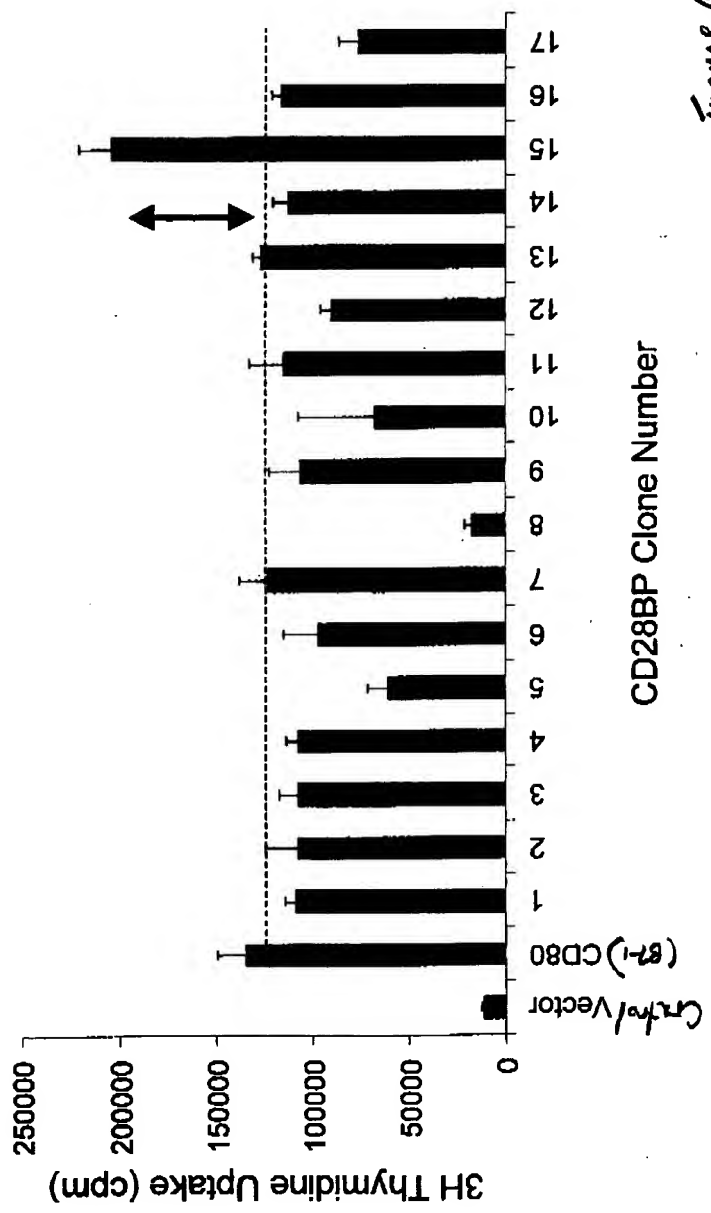
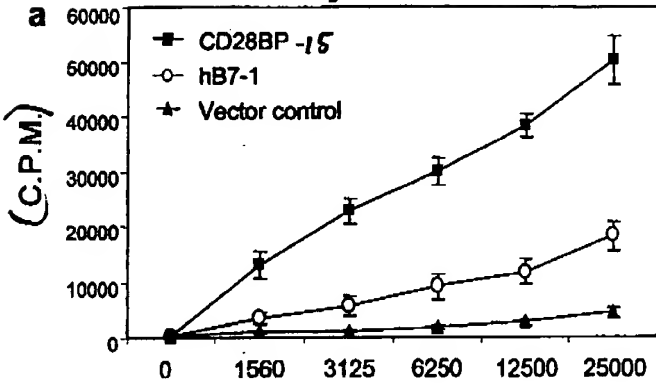


Figure 10

Figures 11A-11C

³H Thymidine Uptake



³H Thymidine Uptake

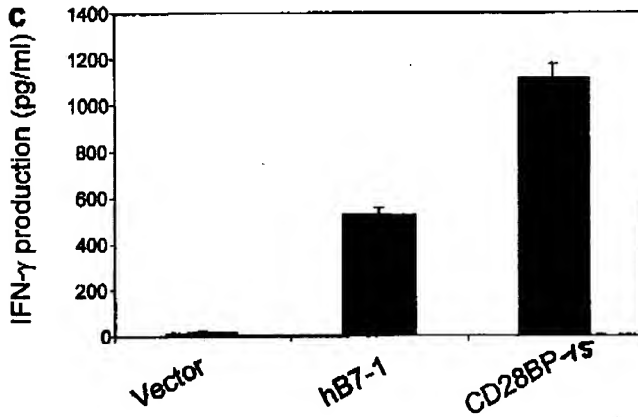
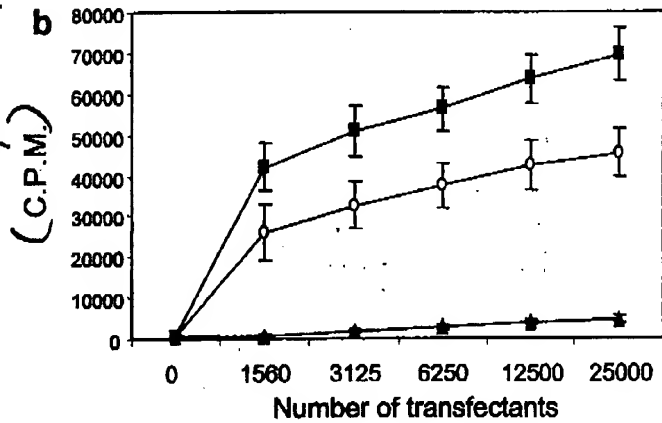
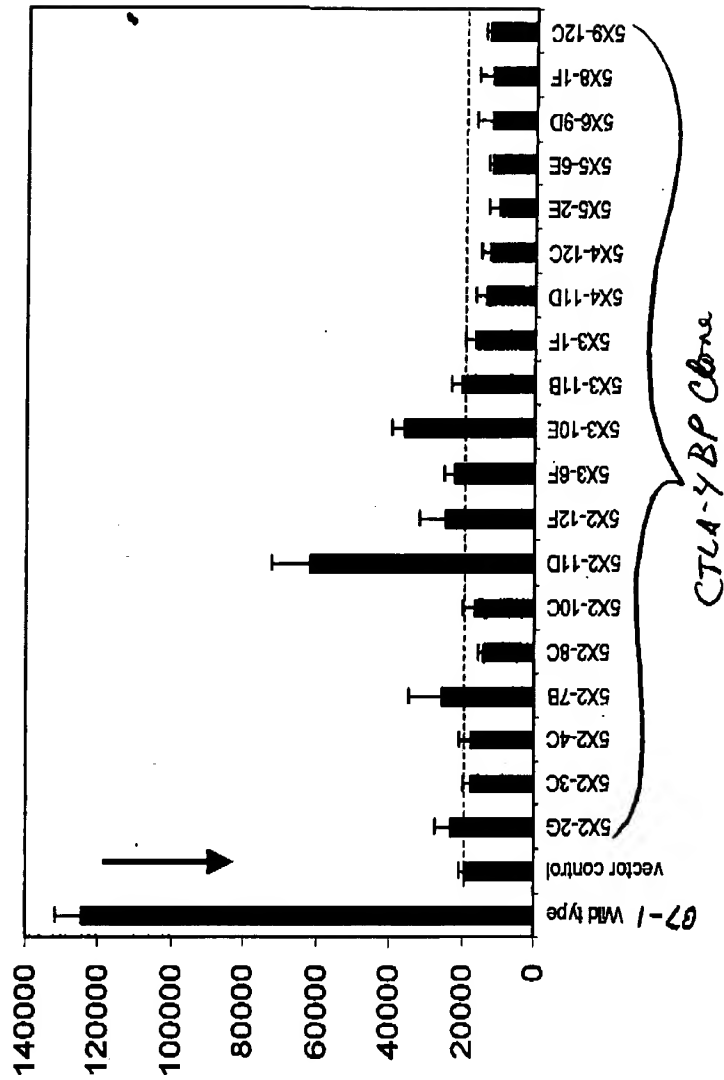


Figure 12

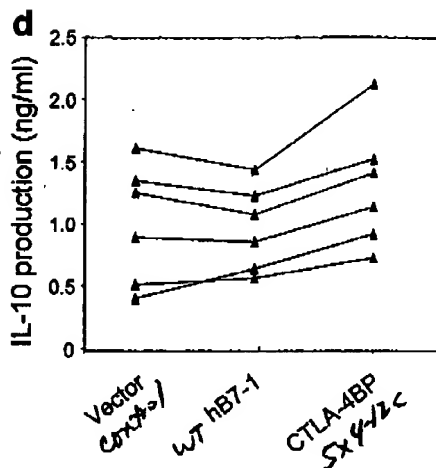
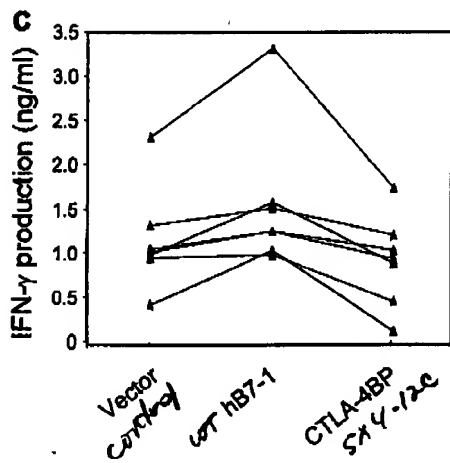
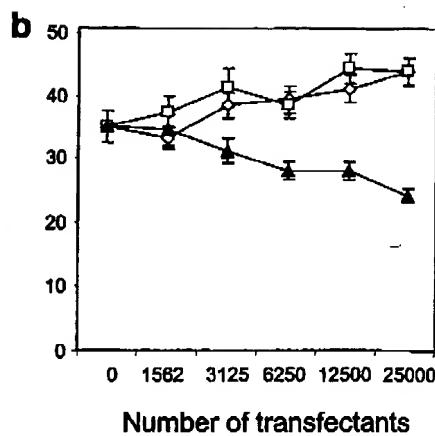
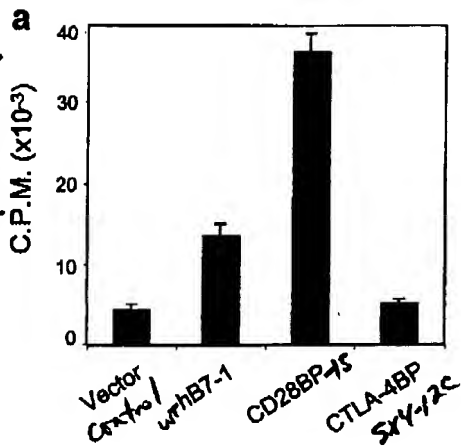
Suppressed T cell Response by CTLA4BP

3H Thymidine Uptake (cpm)



Figures 13A-13D

^3H Thymidine Uptake



102290-1203860

Soluble Forms

A

Human B7.1 sECD

AAAGAPVPYDPLEPPR AAHHHHHH



Signal	Extracellular Domain	E-epitope His-tag
(1- 34)	(35-242)	(243-259) (260-268)

B Human B7.1 ECD-Ig Form

BstII hinge -CH2-CH3



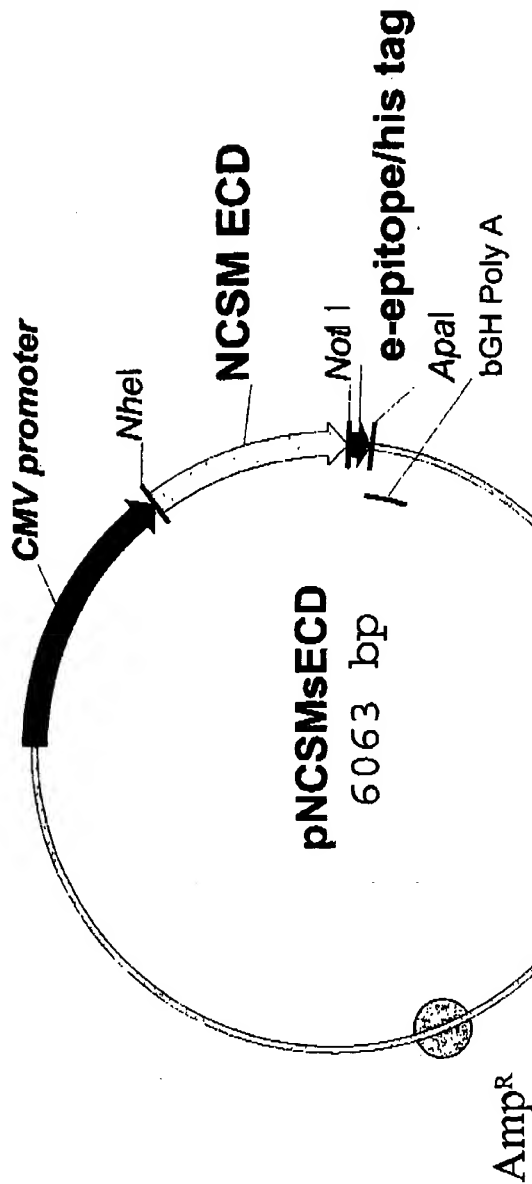
B7.1 ECD (35-242)

Human IgG1 Fc Fragment
GenBank Acc.# P01857
Factor X_a

14A - 14B

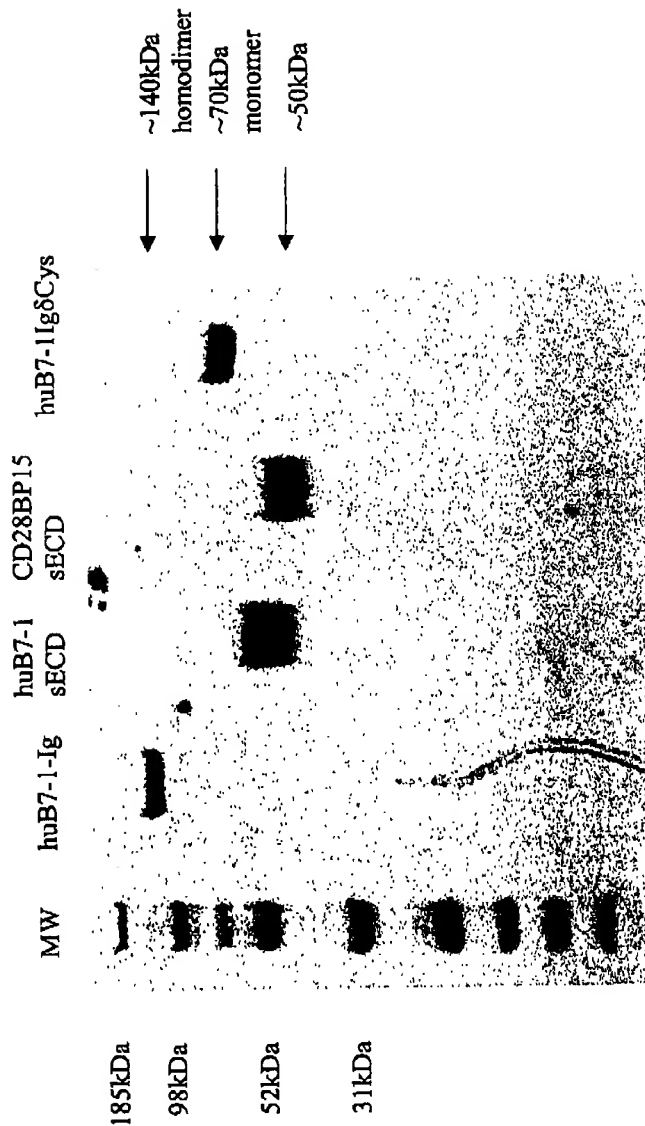
Figures

NCSM-sECD Expression Construct



15
Figure 10

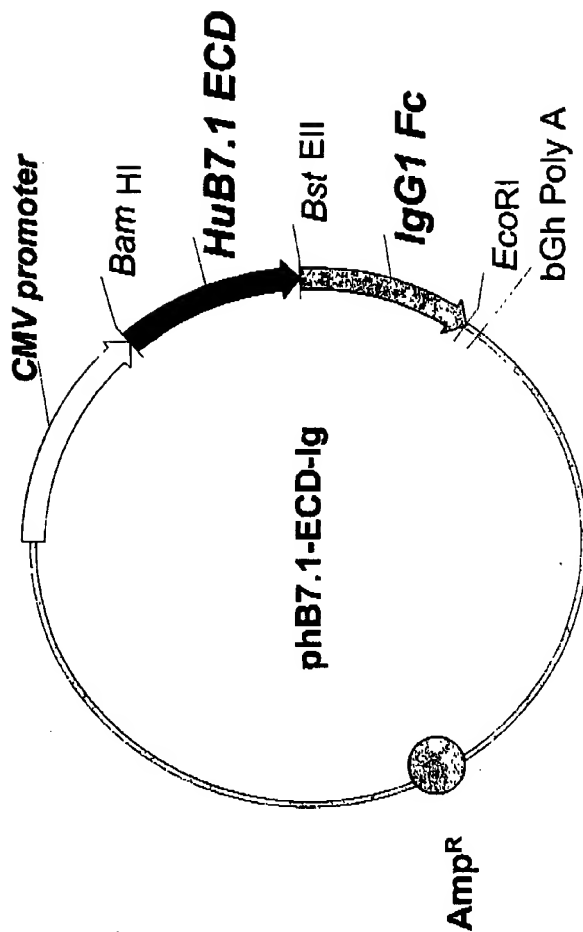
SDS-PAGE showing various soluble forms of wt & NCSM proteins



16
Figure 1

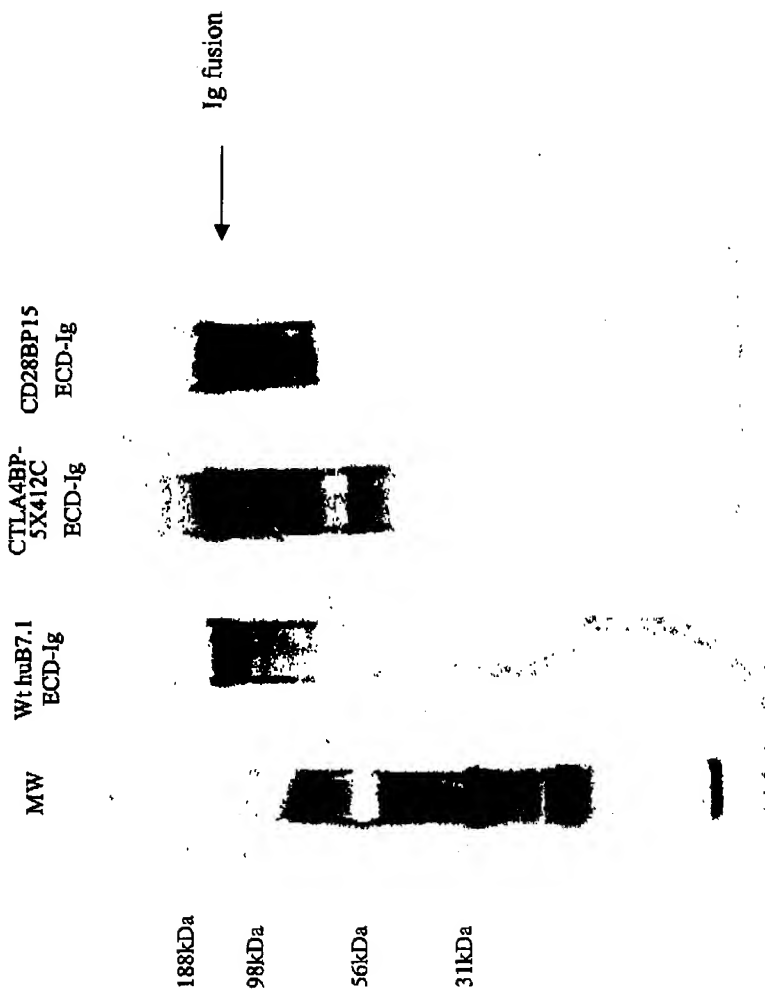
102290"42E8880

B7-1-ECD-Ig Fusion Expression Construct



17
Figure 1

Scale-up Production of wild-type soluble Human B7.1-, CTLA4BP 5X4-12C-, and CD28BP-15 ECD-Ig Fusion Proteins



Expression of CTLA-4-BP-Ig and CD28-BP-Ig Proteins

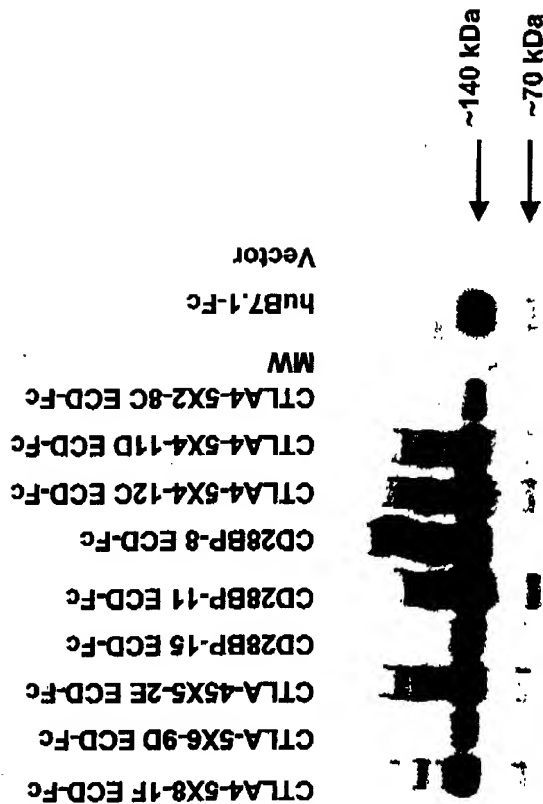
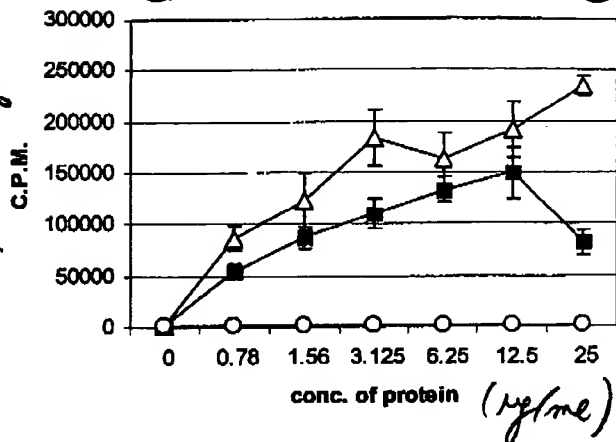
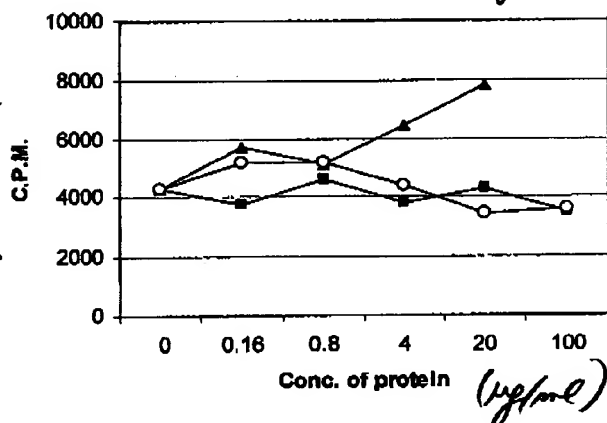
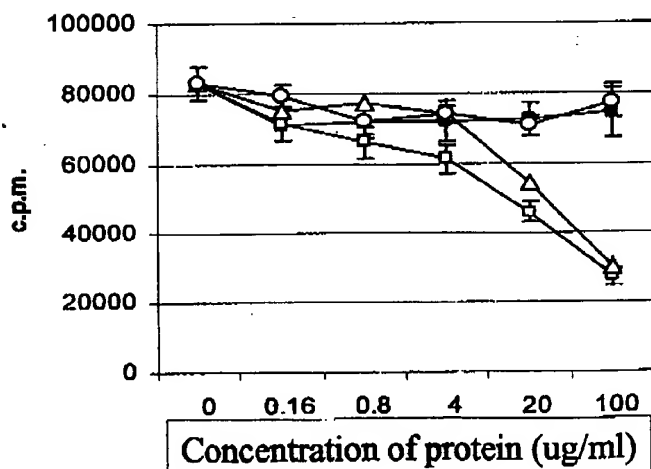


Figure 1

(a) ^3H -thymidine Uptake

Figures 20A - 20C

(b) ^3H -thymidine Uptake(c) ^3H -thymidine Uptake

(d)

³H thymidine Uptake

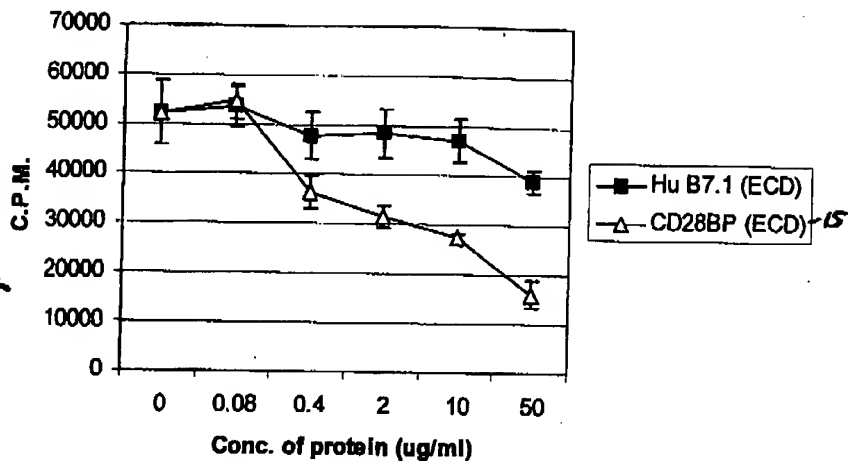
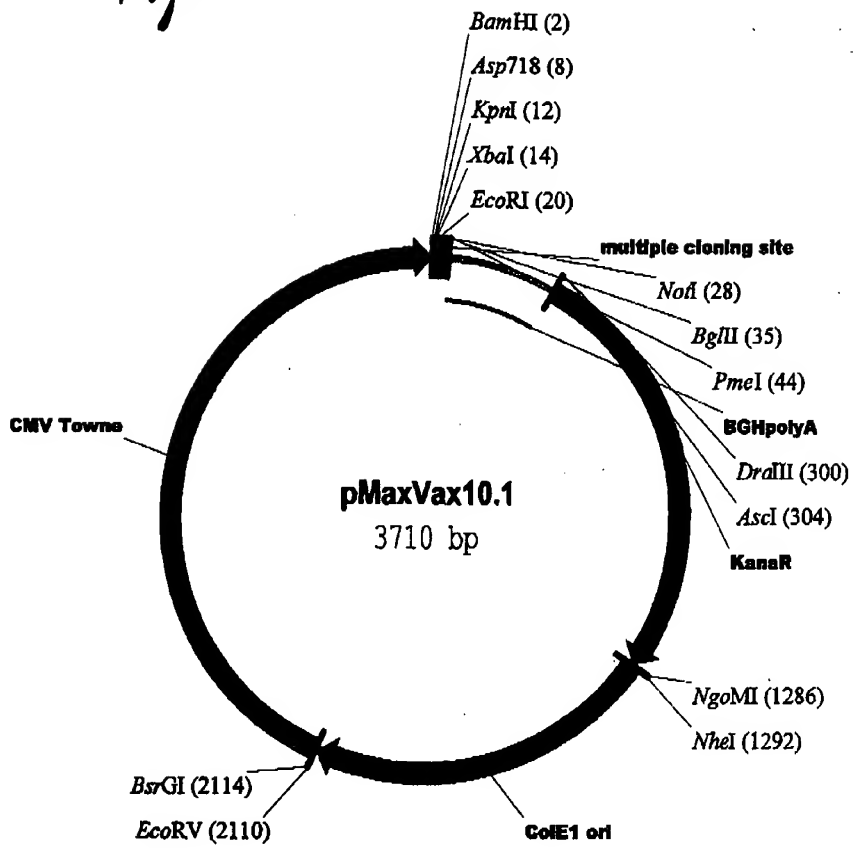


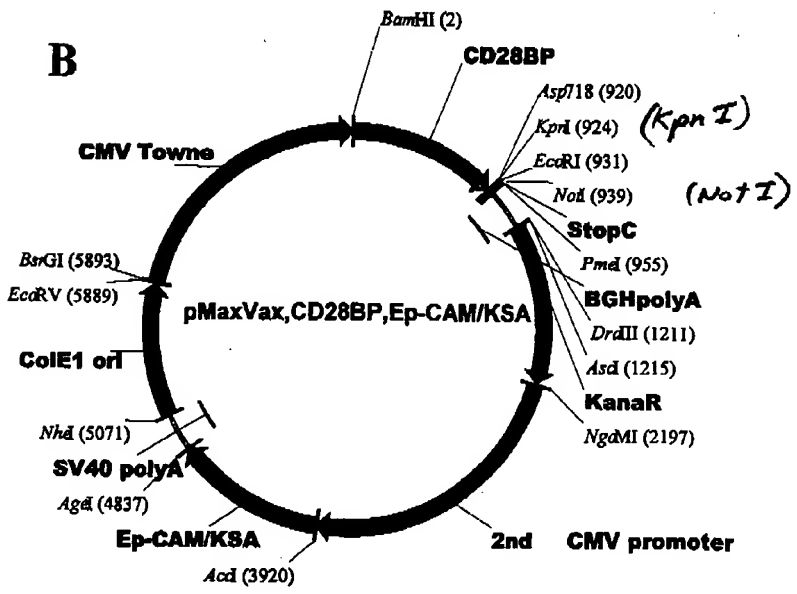
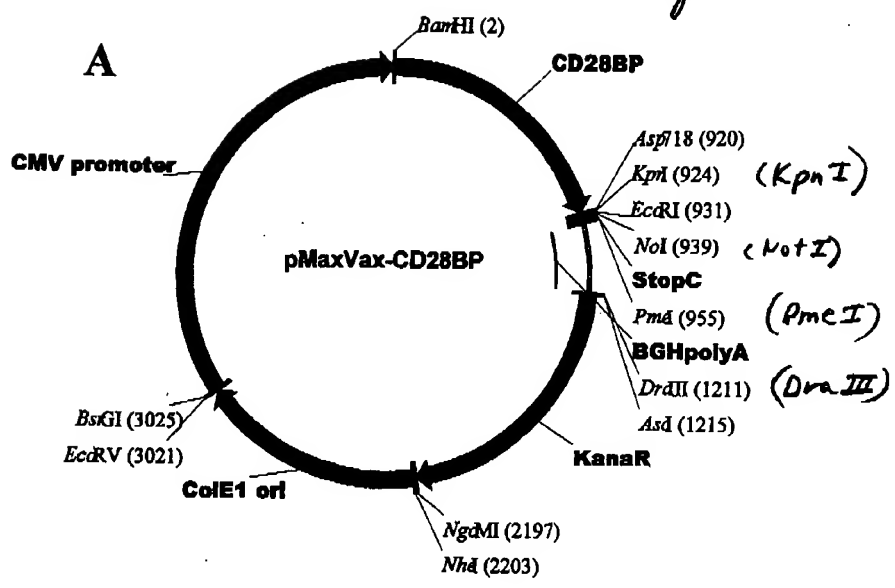
Figure 20D

Figure 21



0988324.062201

Figures 22A-22B



0988324-062201